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Protein



Ligands



Prot. pr.

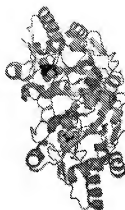
Periplasmic binding protein



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Protein chains

229 a.a.

Ligands

ELC x2

Waters x349

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AstexViewer™@MSD-EBI

Run PROCHECK

Clefts Calculation

PDB id: 2hxw

Name: Periplasmic binding protein

Title: Crystal structure of peb3 from campylobacter jejuni

Structure: Major antigenic peptide peb3. Chain: a, b. Engineered: ye.

Source: Campylobacter jejuni. Strain: nctc 11168. Gene: peb3. Ex: escherichia coli.

UniProt: Chains A, B: Q0PBL7 (Q0PBL7_CAMJE) Pfam

Seq: 250

Struc: 229

Key: PfamA domain Secondary structure

Resolution: 1.60Å

R-factor: 0.188

R-free: 0.212

Authors: E.S.Rangarajan, S.Bhatia, D.C.Watson, C.Munger, M.Cyglier, A.Matte, N.M.Young, Montreal-Kingston Bacterial Structural Initiative (Bsgi)

Key ref: E.S.Rangarajan et al. (2007). Structural context for protein glycosylation in bacteria: The structure of PEB3, an adhesin Campylobacter jejuni. *Protein Sci*, 16, 990-995.

[PubMed id: 17456748] [DOI: 10.1110/p.s.062737507]

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Key
Protein Sci 16:95

Structural context for protein N-glycosylation in bacteria: The structure of PEB3, an adhesin from *Campylobacter jejuni*.

E.S.Rangarajan, S.Bhatia, D.C.Watson, C.Munger, M.Cygier, A.Matte, N.M.Young.

ABSTRACT

Campylobacter jejuni is unusual among bacteria in possessing a eukaryotic-like system for N-linked protein glycosylation residues in sequons of the type Asp/Glu-Xaa-Asn-Xaa-Ser/Thr. However, little is known about the structural context of glycosylated sequons, limiting the design of novel recombinant glycoproteins. To obtain more information on sequon structure we have determined the crystal structure of the PEB3 (Cj0289c) dimer. PEB3 has the class II periplasmic-binding protein with each monomer having two domains with a ligand-binding site containing citrate located between them, and overall resembles molybdate- and sulfate-binding proteins. The sequon around Asn90 is located within a surface-exposed loop of two structural elements. The three key residues are well exposed on the surface; hence, they may be accessible to the oligosaccharyltransferase in the folded state.

Selected figure(s)



Figure 2.

Figure 2. PEB3-binding site and sequon structure. (A) Citrate binding-site density, 2Fo-FC (omit) electron density map contour.

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Literature references that cite this PDB file's key reference

PubMed id Reference

- 18318380 T.D.Ho, B.M.Davis, J.M.Ritchie, and M.K.Waidor (2008).
 Type 2 secretion promotes enterohemorrhagic *Escherichia coli* adherence and intestinal colonization.
Infect Immun, 76, 1858-1865.

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